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(FILE 'HOME' ENTERED AT 16:10:50 ON 26 DEC 2002)

FILE 'CAPLUS' ENTERED AT 16:22:23 ON 26 DEC 2002

L1 94394 S NAD##  
L2 4559 S NAD(W)P  
L3 4 S L2 AND CONFIGURATION AND (BIND? OR BOUND) AND (PEPTIDE OR POL  
L4 95 S L2 (3A) (PEPTIDE OR POLYPEPTIDE OR PROTEIN)  
L5 40 S L4 AND (CONFORM? OR STRUCTURE OR BIND?)  
L6 35 S L5 NOT MECHANISM  
L7 34 S L6 NOT (KINASE C)  
L8 30 S L7 NOT RNA

=> d bib,kwic 1-30

L8 ANSWER 1 OF 30 CAPLUS COPYRIGHT 2002 ACS  
AN 2002:799342 CAPLUS  
TI Optical tomography of human skin with subcellular spatial and picosecond  
time resolution using intense near infrared femtosecond laser pulses  
AU Koenig, Karsten; Wollina, Uwe; Riemann, Iris; Peukert, Christiane;  
Halbhuber, Karl-Juergen; Konrad, Helga; Fischer, Peter; Fuenfstueck,  
Veronika; Fischer, Tobias W.; Elsner, Peter  
CS Laser Microscopy Div., Inst. Anatomy II, Univ. Jena, Jena, D-07740,  
Germany  
SO Proceedings of SPIE-The International Society for Optical Engineering  
(2002), 4620 (Multiphoton Microscopy in the Biomedical Sciences II),  
191-201  
CODEN: PSISDG; ISSN: 0277-786X  
PB SPIE-The International Society for Optical Engineering  
DT Journal  
LA English  
RE.CNT 16 THERE ARE 16 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT  
AB We describe the novel high resoln. imaging tool DermaInspect 100 for  
non-invasive diagnosis of dermatol. disorders based on multiphoton  
autofluorescence imaging (MAI) and second harmonic generation. Femtosecond  
laser pulses in the spectral range of 750 nm to 850 nm have been used to  
image in vitro and in vivo human skin with subcellular spatial and  
picosecond temporal resoln. The non-linear induced autofluorescence  
originates mainly from naturally endogenous fluorophores/**protein**  
**structures** like NAD(P)H, flavins, keratin,  
collagen, elastin, porphyrins and melanin. Second harmonic generation was  
obsd. in the stratum corneum and in the dermis. The system with a  
wavelength-tunable compact 80 MHz Ti:sapphire laser, a scan module with  
galvo scan mirrors, piezoelec. objective positioner, fast photon detector  
and time-resolved single photon counting unit was used to perform optical  
sectioning and 3D autofluorescence lifetime imaging (t-mapping). In  
addn., a modified femtosecond laser scanning microscope was involved in  
autofluorescence measurements. Tissues of patients with psoriasis, nevi,  
dermatitis, basaloma and melanoma have been investigated. Individual  
cells and skin **structures** could be clearly visualized.  
Intracellular components and connective tissue **structures** could  
be further characterized by tuning the excitation wavelength in the range  
of 750 nm to 850 nm and by calcn. of mean fluorescence lifetimes per pixel  
and of particular regions of interest. The novel non-invasive imaging  
system provides 4D (x,y,z,t) optical biopsies with subcellular resoln. and  
offers the possibility to introduce a further optical diagnostic method in  
dermatol.  
  
L8 ANSWER 2 OF 30 CAPLUS COPYRIGHT 2002 ACS  
AN 2002:603004 CAPLUS  
DN 137:306454  
TI Molecular cloning and characterization of the gene coding for the aerobic

azoreductase from *Xenophilus azovorans* KF46F  
AU Blumel, Silke; Knackmuss, Hans-Joachim; Stolz, Andreas  
CS Institut fur Mikrobiologie der Universitat Stuttgart, Stuttgart, 70569,  
Germany  
SO Applied and Environmental Microbiology (2002), 68(8), 3948-3955  
CODEN: AEMIDF; ISSN: 0099-2240  
PB American Society for Microbiology  
DT Journal  
LA English

RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB The gene coding for an aerobic azoreductase was cloned from *Xenophilus azovorans* KF46F (formerly *Pseudomonas* sp. strain KF46F), which was previously shown to grow with the carboxylated azo compd. 1-(4'-carboxyphenylazo)-2-naphthol (carboxy-Orange II) as the sole source of carbon and energy. The deduced amino acid sequence encoded a protein with a mol. wt. of 30,278 and showed no significant homol. to amino acid sequences currently deposited at the relevant data bases. A presumed NAD(P)H-binding site was identified in the amino-terminal region of the azoreductase. The enzyme was heterologously expressed in *Escherichia coli* and the azoreductase activities of resting cells and cell exts. were compared. The results suggested that whole cells of the recombinant *E. coli* strains were unable to take up sulfonated azo dyes and therefore did not show in vivo azoreductase activity. The turnover of several industrially relevant azo dyes by cell exts. from the recombinant *E. coli* strain was demonstrated.

IT Protein motifs  
(NAD(P)H-binding site; mol. cloning and  
characterization of the gene coding for the aerobic azoreductase from  
*Xenophilus azovorans* KF46F)

L8 ANSWER 3 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2002:145298 CAPLUS

TI Comparison of Human Chromosome 6p25 with Mouse Chromosome 13 Reveals a Greatly Expanded Ov-Serpin Gene Repertoire in the Mouse

AU Kaiserman, Dion; Knaggs, Susan; Scarff, Katrina L.; Gillard, Anneliese; Mirza, Ghazala; Cadman, Matthew; McKeone, Richard; Denny, Paul; Cooley, Jessica; Benarafa, Charaf; Remold-O'Donnell, Eileen; Ragoussis, Jiannis; Bird, Phillip I.

CS Department of Biochemistry and Molecular Biology, Monash University, 3800, Australia

SO Genomics (2002), 79(3), 349-362

CODEN: GNMCEP; ISSN: 0888-7543

PB Academic Press

DT Journal

LA English

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB Ov-serpins are intracellular proteinase inhibitors implicated in the regulation of tumor progression, inflammation, and cell death. The 13 human ov-serpin genes are clustered at 6p25 (3 genes) and 18q21 (10 genes), and share common structures. We show here that a 1-Mb region on mouse chromosome 13 contains at least 15 ov-serpin genes compared with the three ov-serpin genes within 0.35 Mb at human 6p25 (SERPINB1 (MNEI), SERPINB6 (PI-6), SER-PINB9 (PI-9)). The mouse serpins have characteristics of functional inhibitors and fall into three groups on the basis of similarity to MNEI, PI-6, or PI-9. The genes map between the mouse orthologs of the Werner helicase interacting protein and NAD(P)H menadioine oxidoreductase 2 genes, in a region that contains the markers D13Mit136 and D13Mit116. They have the seven-exon structure typical of human 6p25 ov-serpin genes, with identical intron phasing. Most show restricted patterns of expression, with common sites of synthesis being the placenta and immune tissue. Compared with human, this larger mouse serpin repertoire probably reflects

the need to regulate a larger proteinase repertoire arising from differing evolutionary pressures on the reproductive and immune systems. (c) 2002 Academic Press.

L8 ANSWER 4 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2001:267358 CAPLUS

DN 135:15850

TI NAD(P)H:menadione oxidoreductase of the amitochondriate eukaryote *Giardia lamblia*: a simpler homologue of the vertebrate enzyme

AU Sanchez, Lidya B.; Elmendorf, Heidi; Nash, Theodore E.; Muller, Miklos  
CS Laboratory of Biochemical Parasitology, The Rockefeller University, New York, NY, 10021, USA

SO Microbiology (Reading, United Kingdom) (2001), 147(3), 561-570  
CODEN: MROBEO; ISSN: 1350-0872

PB Society for General Microbiology

DT Journal

LA English

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB The amitochondriate eukaryote *Giardia lamblia* contains an NAD(P)H:menadione oxidoreductase (EC 1.6.99.2) (glQR) that catalyzes the two-electron transfer oxidn. of NAD(P)H with a quinone as acceptor. The gene encoding this protein in *G. lamblia* was expressed in *Escherichia coli*. The purified recombinant protein had an NAD(P)H oxidoreductase activity, with NADPH being a more efficient electron donor than NADH. Menadione, naphthoquinone and several artificial electron acceptors served as substrate for the enzyme. The glQR protein shows high amino acid similarity to its homologs in vertebrates and also to a series of hypothetical proteins from bacteria. Although glQR is considerably smaller than the mammalian enzymes, three-dimensional modeling shows similar arrangement of the secondary structural elements. Most amino acid residues of the mammalian enzymes that participate in substrate binding or catalysis are conserved. Conservation of these features and the similarity in substrate specificity and in susceptibility to inhibitors establish glQR as an authentic member of this protein family.

IT Enzyme functional sites

(active; active site structure of menadione:oxidoreductase of *Giardia lamblia*)

IT Mammal (Mammalia)

(conservation of secondary structure of NAD(P)H menadione:oxidoreductases of *Giardia lamblia* and mammals)

IT Evolution

(mol., conservative; conservation of secondary structure of NAD(P)H menadione:oxidoreductases of *Giardia lamblia* and mammals)

IT Secondary structure

(protein; conservation of secondary structure of NAD(P)H menadione:oxidoreductases of *Giardia lamblia* and mammals)

L8 ANSWER 5 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2000:615952 CAPLUS

DN 134:15548

TI Molecular characterization and localization of the NAD(P)H oxidase components gp91-phox and p22-phox in endothelial cells

AU Bayraktutan, Ulvi; Blayney, Lynda; Shah, Ajay M.

CS Departments of Cardiology, King's College, London, SE5 9PJ, UK

SO Arteriosclerosis, Thrombosis, and Vascular Biology (2000), 20(8), 1903-1911

CODEN: ATVBFA; ISSN: 1079-5642

PB Lippincott Williams & Wilkins

DT Journal

LA English

RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB The prodn. of reactive oxygen species (ROS) within endothelial cells may have several effects, including alterations in the activity of paracrine factors, gene expression, apoptosis, and cellular injury. Recent studies indicate that a phagocyte-type NAD(P)H oxidase is a major source of endothelial ROS. In contrast to the high-output phagocytic oxidase, the endothelial enzyme has much lower biochem. activity and a different substrate specificity (NADH>NADPH). In the present study, we (1) cloned and characterized the cDNA and predicted amino acid **structures** of the 2 major subunits of rat coronary microvascular endothelial cell NAD(P)H oxidase, gp91-phox and p22-phox; (2) undertook a detailed comparison with phagocytic NADPH oxidase sequences; and (3) studied the subcellular location of these subunits in endothelial cells. Although these studies revealed an overall high degree of homol. (>90%) between the endothelial and phagocytic oxidase subunits, the endothelial gp91-phox sequence has potentially important differences in a putative NADPH-binding domain and in putative glycosylation sites. In addn., the subcellular location of the endothelial gp91-phox and p22-phox subunits is significantly different from that reported for the neutrophil oxidase, in that they are predominantly intracellular and collocated in the vicinity of the endoplasmic reticulum. This first detailed characterization of gp91-phox and p22-phox **structure** and location in endothelial cells provides new data that may account, in part, for the differences in function between the phagocytic and endothelial NAD(P)H oxidases.

IT **Protein sequences**

cDNA sequences

(of endothelial NAD(P)H oxidases of rat; mol. characterization and subcellular localization of NAD(P)H oxidase components gp91-phox and p22-phox in vascular endothelial cells)

L8 ANSWER 6 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2000:444725 CAPLUS

DN 133:306968

TI Analysis of functional domains on glutamate synthase

AU Nalbantoglu, Barbaros

CS Department of Biochemistry, Faculty of Sciences and Arts, Ataturk University, Erzurum, Turk.

SO Turkish Journal of Biology (2000), 24(2), 197-213

CODEN: TJBIEZ; ISSN: 1300-0152

PB Scientific and Technical Research Council of Turkey

DT Journal; General Review

LA English

RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB A review with 56 refs. Glutamate synthases (GOGAT) were analyzed to identify the functional **binding** domains of the substrate (glutamine) and cofactors (FMN, NAD(P)H, FAD, [3Fe-4S]1+,0 and [4Fe-4S]2+,1+ clusters and ferredoxin) on this enzyme. The published amino acid sequences of six different NAD(P)H-dependent GOGATs (NAD(P)H-GOGAT) and ten different ferredoxin-dependent GOGATs (Fd-GOGAT) were used for this anal. The amino acid sequences of these sixteen GOGATs were compared with the amino acid sequences of aminotransferases for glutamine, flavoproteins for FMN, flavoproteins and pyridine-nucleotide-dependent enzymes for FAD and NAD(P)H, iron-sulfur **proteins** for [3Fe-4S]1+,0 and [4Fe-4S]2+,1+ clusters and ferredoxin-dependent enzymes for ferredoxin. It was detd. that Fd-GOGAT has one domain each for glutamine, FMN and [3Fe-4S]1+,0 cluster and two domains each for FAD and ferredoxin; the NADPH-GOGAT .alpha. subunit has the same domains as Fd-GOGAT except for the ferredoxin domains, and .beta. subunit has one domain each for NADPH and FAD and two domains for two [4Fe-4S]2+,1+ clusters; NADH-GOGAT has the same domains as NADPH-GOGAT.

L8 ANSWER 7 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2000:404875 CAPLUS

DN 133:147280

TI New functions for the ancient globin family: bacterial responses to nitric oxide and nitrosative stress  
AU Poole, Robert K.; Hughes, Martin N.  
CS Krebs Inst. Biomol. Res., Univ. Sheffield, Sheffield, S10 2TN, UK  
SO Molecular Microbiology (2000), 36(4), 775-783  
CODEN: MOMIEE; ISSN: 0950-382X  
PB Blackwell Science Ltd.  
DT Journal; General Review  
LA English

RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

AB A review with 36 refs. Globin-like O2-binding proteins occur in bacteria, yeasts and other fungi, and protozoa. The simplest contain protoheme as sole prosthetic group, but show considerable variation in their similarity to the classical animal globins and plant globins. Flavohbs comprise a heme domain homologous to classical globins and a ferredoxin-NADP+ reductase (FNR)-like domain that converts the globin into an NAD(P)H-oxidizing protein with diverse reductase activities. In Escherichia coli, the prototype flavoHb (Hmp) is clearly involved in responses to NO and nitrosative stress: (i) the structural gene hmp is upregulated by NO and nitrosating agents; (ii) purified Hmp binds NO avidly, but also converts it to NO3- (aerobically) or N2O (anaerobically); (iii) hmp mutants are hypersensitive to NO and nitrosative stresses. Here, recent advances in E. coli and the growing no. of microbes in which globins are known are reviewed, with particular attention to the essential chem. of NO and related reactive spp., and their interactions with globins, and it is suggested that microbial globins have addnl. functions unrelated to "NO" stresses.

L8 ANSWER 8 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2000:270487 CAPLUS

DN 133:1100

TI 5-Hydroxytryptamine1A receptor/Gi.beta..gamma. stimulates mitogen-activated protein kinase via NAD(P)H oxidase and reactive oxygen species upstream of Src in Chinese hamster ovary fibroblasts

AU Mukhin, Yurii V.; Garnovskaya, Maria N.; Collinsworth, Georgiann; Grewal, Jasjit S.; Pendergrass, DeKisha; Nagai, Toshio; Pinckney, Stephen; Greene, Eddie L.; Raymond, John R.

CS Department of Medicine, Medical University of South Carolina, Charleston, SC, 29425, USA

SO Biochemical Journal (2000), 347(1), 61-67

CODEN: BIJOAK; ISSN: 0264-6021

PB Portland Press Ltd.

DT Journal

LA English

RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI 5-Hydroxytryptamine1A receptor/Gi.beta..gamma. stimulates mitogen-activated protein kinase via NAD(P)H oxidase and reactive oxygen species upstream of Src in Chinese hamster ovary fibroblasts

IT G proteins (guanine nucleotide-binding proteins)  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(Gi (adenylate cyclase-inhibiting); 5-hydroxytryptamine1A receptor coupled to Gi.beta..gamma. stimulates MAP kinase via NAD(P)H oxidase and reactive oxygen species upstream of Src in Chinese hamster ovary fibroblasts)

L8 ANSWER 9 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 2000:26761 CAPLUS

DN 132:148287

TI New sequence motifs in flavoproteins: evidence for common ancestry and

tools to predict **structure**

AU Vallon, Olivier

CS Institute de Biologie Physico-Chimique, CNRS, Paris, F-75005, Fr.

SO Proteins: Structure, Function, and Genetics (2000), 38(1), 95-114  
CODEN: PSFGY; ISSN: 0887-3585

PB Wiley-Liss, Inc.

DT Journal

LA English

RE.CNT 104 THERE ARE 104 CITED REFERENCES AVAILABLE FOR THIS RECORD  
ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI New sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**

AB We describe two new sequence motifs, present in several families of flavoproteins. The "GG motif" (RxGGRxxS/T) is found shortly after the .beta..alpha..beta.dinucleotide-binding motif (DBM) in L-amino acid oxidases, achacin and aplysianin-A, monoamine oxidases, corticosteroid-binding proteins, and tryptophan 2-monooxygenases. Other disperse sequence similarities between these families suggest a common origin. AGG motif is also found in protoporphyrinogen oxidase and carotenoid desaturases and, reduced to the central GG doublet, in the TH14 protein, dTDP-4-dehydrorhamnose reductase, sol. fumarate reductase, steroid dehydrogenases, Rab GDP-dissocn. inhibitor, and in most flavoproteins with two dinucleotide-binding domains (glutathione reductase, glutamate synthase, flavin-contg. monooxygenase, trimethylamine dehydrogenase...). In the latter families, an "ATG motif" (oxhhhATG) is found in both the FAD- and NAD(P)H-binding domains, forming the fourth .beta.-strand of the Rossman fold and the connecting loop. On the basis of these and previously described motifs, we present a classification of dinucleotide-binding proteins that could also serve as an evolutionary scheme. Like the DBM, the ATG motif appears to predate the divergence of NAD(P)H- and FAD-binding proteins. We propose that flavoproteins have evolved from a well-differentiated NAD(P)H-binding protein. The bulk of the substrate-binding domain was formed by an insertion after the fourth .beta.-strand, either of a closely related NAD(P)H-binding domain or of a domain of completely different origin.

IT Proteins, specific or class  
RL: PRP (Properties)  
(FAD-binding; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Proteins, specific or class  
RL: PRP (Properties)  
(NAD(P)H-binding; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Proteins, specific or class  
RL: PRP (Properties)  
(Rossman-type; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Proteins, specific or class  
RL: PRP (Properties)  
(dinucleotide-binding; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Enzymes, properties  
RL: PRP (Properties)  
(flavin-contg.; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Protein sequences  
(homol.; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Evolution  
(mol.; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Protein motifs  
 (new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Flavoproteins  
 RL: PRP (Properties)  
 (new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT **Conformation**  
 (protein; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT Enzyme functional sites  
 (substrate-**binding**; new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

IT 9035-82-9, Dehydrogenase 9038-14-6, Flavin-contg. monooxygenase  
 RL: PRP (Properties)  
 (new sequence motifs in flavoproteins: evidence for common ancestry and tools to predict **structure**)

L8 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1999:286792 CAPLUS

DN 131:99211

TI **Crystal structure** of NAD(P)H:flavin oxidoreductase from *Escherichia coli*

AU Ingelman, Margareta; Ramaswamy, S.; Niviere, Vincent; Fontecave, Marc; Eklund, Hans

CS Department of Molecular Biology, Swedish University of Agricultural Sciences Biomedical Center, Uppsala, S-751 24, Swed.

SO Biochemistry (1999), 38(22), 7040-7049

CODEN: BICHAW; ISSN: 0006-2960

PB American Chemical Society

DT Journal

LA English

RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI **Crystal structure** of NAD(P)H:flavin oxidoreductase from *Escherichia coli*

AB Flavon reductases use flavins as substrates and are distinct from flavoenzymes which have tightly bound flavins. The reduced flavin can serve to reduce ferric complexes and Fe proteins. In *E. coli*, reactivation of ribonucleotide reductase is achieved by reduced flavins produced by flavin reductase. The **crystal structure** of *E. coli* NAD(P)H-flavin reductase detd. here revealed that the enzyme **structure** was similar to the **structures** of the ferredoxin reductase family of flavoproteins despite very low sequence similarities. The main difference between the flavin reductase and structurally related flavoproteins was that there was no **binding** site for the AMP moiety of FAD. The direction of the helix in the flavin **binding** domain, corresponding to the phosphate **binding** helix in the flavoproteins, was also slightly different and less suitable for phosphate **binding**. The interactions for flavin substrates were instead provided by a hydrophobic isoalloxazine **binding** site that also contained a Ser and a Thr residue, which formed H-bonds to the isoalloxazine of bound riboflavin in a substrate complex.

ST flavin reductase **crystal structure** *Escherichia*

IT *Escherichia coli*

(**crystal structure** of NAD(P)H-flavin reductase from *Escherichia coli*)

IT Crystal growth

**Crystal structure**

(of NAD(P)H-flavin reductase from *Escherichia coli*)

IT **Conformation**

(protein; of NAD(P)H-flavin reductase from *Escherichia coli*)

IT 64295-83-6, NAD(P)H-flavin reductase

RL: PEP (Physical, engineering or chemical process); PRP (Properties);  
PROC (Process)  
(crystal **structure** of NAD(P)H-flavin reductase from  
Escherichia coli)

L8 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1998:422047 CAPLUS

DN 129:158428

TI New insights for dinucleotide backbone **binding** in conserved  
C5'-H... O hydrogen bonds

AU Chu, Pei-Ying; Hwang, Ming-Jing

CS Division of Structural Biology, Inst. Biomed. Sci., Inst. Biomedical Sci.,  
Taipei, Taiwan

SO Journal of Molecular Biology (1998), 279(4), 695-701

CODEN: JMOBAK; ISSN: 0022-2836

PB Academic Press Ltd.

DT Journal

LA English

RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD

ALL CITATIONS AVAILABLE IN THE RE FORMAT

TI New insights for dinucleotide backbone **binding** in conserved  
C5'-H... O hydrogen bonds

~~AB~~ Most enzymes that utilize dinucleotide NAD or NADP are known to comprise a  
glycine-rich loop segment (e.g. the GXGXXG signature motif of Rossman  
fold) which **binds** the cofactor's diphosphate moiety. Through  
anal. of a set of diverse **NAD(P)**-bound **protein**  
**structures**, we show here that with few exceptions this diphosphate  
**binding** is complemented by a second loop segment interacting from  
a different angle with unconventional yet apparently ubiquitous C-H...O  
hydrogen bonds formed between C5' methylene of dinucleotide and,  
primarily, carbonyl oxygen of protein. This finding implicates an  
important role of C5' in protein-nucleotide recognition.

IT Enzyme functional sites

(cofactor-**binding**; unconventional hydrogen bonding in  
nicotinamide dinucleotide cofactor recognition by enzymes)

L8 ANSWER 12 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1997:584258 CAPLUS

DN 127:259159

TI Identifying the major proteome components of Haemophilus influenzae  
type-strain NCTC 8143

AU Link, Andrew J.; Hays, Lara G.; Carmack, Edwin B.; Yates, John R., III

CS Dep. Molecular Biotechnology, Washington Univ., Seattle, WA, 98195, USA

SO Electrophoresis (1997), 18(8), 1314-1334

CODEN: ELCTDN; ISSN: 0173-0835

PB Wiley-VCH

DT Journal

LA English

IT Proteins, specific or class

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP  
(Properties); BIOL (Biological study); OCCU (Occurrence)

(ATP-**binding**, Methylgalactoside permease ATP-**binding**  
protein; proteins of Haemophilus influenzae type-strain NCTC 8143,  
sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP  
(Properties); BIOL (Biological study); OCCU (Occurrence)

(galactoside-**binding**, Periplasmic; proteins of Haemophilus  
influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and  
gene expression)

IT Proteins, specific or class

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP  
(Properties); BIOL (Biological study); OCCU (Occurrence)

(glutamine-**binding**, periplasmic; proteins of Haemophilus



influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
 (phosphate-binding, Periplasmic; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
 (precursor, Major ferric iron binding protein precursor; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT Proteins, specific or class  
 RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
 (ribose-binding, Periplasmic; proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

IT 9000-97-9, Aspartate aminotransferase 9001-18-7, Lipoamide dehydrogenase 9001-48-3, Glutathione reductase 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase 9001-52-9, Fructose-1,6-bisphosphatase 9001-60-9, Lactate dehydrogenase 9001-64-3, Malate dehydrogenase 9001-69-8, Ornithine carbamoyltransferase 9001-83-6, Phosphoglycerate kinase 9013-02-9, Adenylate kinase 9013-10-9, Glucosamine-6-phosphate deaminase 9014-08-8, Enolase 9014-12-4, Polynucleotide phosphorylase 9014-20-4, Pyruvate dehydrogenase 9015-76-3, Methionyl-tRNA formyltransferase 9015-83-2, Phosphoribosylpyrophosphate synthetase 9023-46-5, Threonyl-tRNA synthetase 9023-48-7, Seryl-tRNA synthetase 9023-56-7, CTP synthetase 9023-57-8, Adenylosuccinate synthetase 9023-58-9, Argininosuccinate synthetase 9023-78-3, Triosephosphate isomerase 9023-93-2, Acetyl-coenzyme A carboxylase 9024-00-4, Tryptophanase 9024-32-2, Dihydroxyacid dehydrase 9024-52-6, Fructose-bisphosphate aldolase 9024-82-2, Inorganic pyrophosphatase 9026-39-5, Uridine kinase 9026-69-1, Carbamate kinase 9027-30-9, Aspartase 9027-42-3, Acetate kinase 9027-60-5, N-Acetylneuraminase lyase 9027-73-0, 5'-Nucleotidase 9029-83-8, Serine hydroxymethyltransferase 9030-21-1, Purine-nucleoside phosphorylase 9030-22-2, Uridine phosphorylase 9030-24-4, Uracil phosphoribosyltransferase 9030-66-4, Glycerol kinase 9030-90-4, Phosphoserine aminotransferase 9031-02-1, 2-Oxoglutarate dehydrogenase 9032-29-5, Dihydrolipoamide acetyltransferase 9032-62-6, Phosphoglyceromutase 9032-89-7, Udp-glucose 4-epimerase 9037-18-7, 2',3'-Cyclic-nucleotide 2'-phosphodiesterase 9037-44-9, Exonuclease III 9037-67-6, .gamma.-Aminobutyric acid transaminase 9054-65-3, Branched-chain-amino-acid transaminase 9054-89-1, Superoxide dismutase 9055-59-8, Dihydrodipicolinate synthetase 9055-68-9, Prolyl-tRNA synthetase 9068-29-5, Tetrahydropteroyltrimethyltransferase 9068-76-2, Glutamyl-tRNA synthetase 9074-14-0, Thioredoxin reductase 9075-29-0, Phosphoglycerate dehydrogenase 9075-71-2, Biotin carboxylase 37205-35-9, Arginyl-tRNA synthetase 37250-34-3, 3-Ketoacyl-acyl carrier protein reductase 37290-89-4, Cysteine synthetase 37341-55-2, Phosphoenolpyruvate carboxykinase 54596-29-1, .gamma.-Glutamyl phosphate reductase 64295-83-6, NAD(P)H-flavin oxidoreductase 72162-89-1, tRNA-guanine transglycosylase 76106-82-6, Ribonuclease E 85030-75-7, ADP-L-glycero-D-mannoheptose-6-epimerase 142298-62-2, Short chain alcohol dehydrogenase

RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
 (proteins of Haemophilus influenzae type-strain NCTC 8143, sequence anal., isoelec. point, and gene expression)

DN 127:14789  
 TI NADP-dependent enzymes: I: Conserved stereochemistry of cofactor  
**binding**  
 AU Carugo, Oliviero; Argos, Patrick  
 CS European Molecular Biology Laboratory, Heidelberg, 69012, Germany  
 SO Proteins: Structure, Function, and Genetics (1997), 28(1), 10-28  
 CODEN: PSFGY; ISSN: 0887-3585  
 PB Wiley-Liss  
 DT Journal  
 LA English  
 TI NADP-dependent enzymes: I: Conserved stereochemistry of cofactor  
**binding**  
 AB The ubiquitous redox cofactors, nicotinamide adenine dinucleotides (NAD and NADP), are very similar mols., despite their participation in substantially different biochem. processes. NADP differs from NAD in only the presence of an addnl. phosphate group esterified to the 2'-hydroxyl group of the ribose at the adenine end and yet NADP is confined with few exceptions to the reactions of reductive biosynthesis, whereas NAD is used almost exclusively in oxidative degrdns. The discrimination between NAD and NADP is therefore an impressive example of the power of mol. recognition by proteins. The many known tertiary structures of NADP complexes affords the possibility for an anal. of their discrimination. A systematic anal. of several crystal structures of **NAD(P)-protein** complexes show that: (1) the NADP coenzymes are more flexible in conformation than those of NAD; (2) although the protein-cofactor interactions are largely conserved in the NAD complexes, they are quite variable in those of NADP; and (3) in both cases the pocket around the nicotinamide moiety is substrate dependent. The conserved and variable interactions between protein and cofactors in the resp. **binding** pockets are reported in detail. Discrimination between NAD and NADP is essentially a consequence of the overall pocket and not of a few residues. A clear fingerprint in NAD complexes is a carboxylate side chain that chelates the diol group at the ribose near the adenine, whereas in NADP complexes an arginine side chain faces the adenine plane and interacts with the phosphomonoester. The latter type of interaction might be a general feature of recognition of nucleotides by proteins. Other features such as strand-like hydrogen bonding between the NADP diphosphate moieties and the protein are also significant. The NADP **binding** pocket properties should prove useful in protein engineering and design.

ST enzyme NAD NADP **binding** stereochem  
 IT Enzymes, biological studies  
 RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)  
 (NAD and NADP-dependent; conserved stereochem. of cofactor  
**binding** in NAD(P)-dependent enzymes)  
 IT Enzyme functional sites  
 (cofactor-**binding**; conserved stereochem. of cofactor  
**binding** in NAD(P)-dependent enzymes)  
 IT **Conformation**  
 Molecular recognition  
 (conserved stereochem. of cofactor **binding** in  
 NAD(P)-dependent enzymes)  
 IT 53-59-8, NADP 53-84-9, NAD  
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
 (conserved stereochem. of cofactor **binding** in  
 NAD(P)-dependent enzymes)

L8 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2002 ACS  
 AN 1997:200448 CAPLUS  
 DN 126:260851  
 TI Characterization of the NAD(P)H-plastoquinone-oxidoreductase from maize thylakoid membranes

→ copy in  
 their SDS

AU Funk, Edgar; Steinmueller, Klaus  
 CS Institut fur Entwicklungs- und Molekularbiologie der Pflanzen,  
 Heinrich-Heine-Universitat, Dusseldorf, 40225, Germany  
 SO Photosynthesis: From Light to Biosphere, Proceedings of the International  
 Photosynthesis Congress, 10th, Montpellier, Fr., Aug. 20-25, 1995 (1995),  
 Volume 2, 701-704. Editor(s): Mathis, Paul. Publisher: Kluwer, Dordrecht,  
 Neth.  
 CODEN: 64DFAW  
 DT Conference  
 LA English  
 IT Quaternary **structure**  
 (protein; of NAD(P)H-plastoquinone  
 reductase from maize thylakoid membranes)

L8 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2002 ACS  
 AN 1997:1222 CAPLUS  
 DN 126:101731  
 TI The NADH-binding subunit of respiratory chain complex I is  
 nuclear-encoded in plants and identified only in mitochondria  
 AU Grohmann, Lutz; Rasmusson, Allan G.; Heiser, Volker; Thieck, Oliver;  
 Brennicke, Axel  
 CS Institut Genbiologische Forschung Berlin, Berlin, D-14195, Germany  
 SO Plant Journal (1996), 10(5), 793-803  
 CODEN: PLJUED; ISSN: 0960-7412  
 PB Blackwell  
 DT Journal  
 LA English  
 TI The NADH-binding subunit of respiratory chain complex I is  
 nuclear-encoded in plants and identified only in mitochondria  
 AB In higher plants, genes for subunits of respiratory chain complex I  
 (NADH:ubiquinone oxidoreductase) have so far been identified solely in  
 organellar genomes. At least nine subunits are encoded by the  
 mitochondrial DNA and 11 homologs by the plastid DNA. One of the 'key'  
 components of complex I is the subunit binding the substrate  
 NADH. The corresponding gene for the mitochondrial subunit has now been  
 cloned and identified in the nuclear genome from potato (Solanum  
 tuberosum). The mature protein consists of 457 amino acids and is  
 preceded by a mitochondrial targeting sequence of 30 amino acids. The  
 protein is evolutionarily related to the NADH-binding subunits  
 of complex I from other eukaryotes and is well conserved in the structural  
 domains predicted for binding the substrate NADH, the FMN and  
 one iron-sulfur cluster. Expression examd. in different potato tissues by  
 Northern blot anal. shows the highest steady-state mRNA levels in flowers.  
 Precursor proteins translated in vitro from the cDNA are imported into  
 isolated potato mitochondria in a .DELTA.psi.-dependent manner. The  
 processed translation product has an apparent mol. mass of 55 kDa,  
 identical to the mature protein present in the purified plant  
 mitochondrial complex I. However, the in vitro translated protein is not  
 imported into isolated chloroplasts. To further investigate whether the  
 complex I-like enzyme in chloroplasts contains an analogous subunit for  
 binding of NAD(P)H, different plastid  
 protein fractions were tested with a polyclonal antiserum directed  
 against the bovine 51 kDa NADH-binding subunit. In none of the  
 different thylakoid or stroma protein fractions analyzed were specific  
 cross-reactive polypeptides detected. These results are discussed  
 particularly with respect to the structure of a potential  
 complex I in chloroplasts and the nature of its acceptor site.  
 IT Electron transport system, biological  
 Mitochondria  
 Potato (Solanum tuberosum)  
 Protein sequences  
 cDNA sequences  
 (NADH-binding subunit of respiratory chain complex I is  
 nuclear-encoded in plants and identified only in mitochondria)

IT Gene, plant  
 RL: PRP (Properties)  
 (NADH-binding subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)

IT 9079-67-8, Dehydrogenase, reduced nicotinamide adenine dinucleotide  
 RL: PRP (Properties)  
 (NADH-binding subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)

IT 185830-52-8  
 RL: PRP (Properties)  
 (amino acid sequence; NADH-binding subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)

IT 162486-42-2, GenBank X83999  
 RL: PRP (Properties)  
 (nucleotide sequence; NADH-binding subunit of respiratory chain complex I is nuclear-encoded in plants and identified only in mitochondria)

L8 ANSWER 16 OF 30 CAPLUS COPYRIGHT 2002 ACS  
 AN 1996:573121 CAPLUS  
 DN 125:240912

TI The nicotinamide dinucleotide **binding** motif: a comparison of nucleotide **binding** proteins  
 AU Bellamacina, Cornelia R.  
 CS Rosenstiel Basic Medical Sciences Research Center, Brandeis University, Waltham, MA, 02254-9110, USA  
 SO FASEB Journal (1996), 10(11), 1257-1269  
 CODEN: FAJOEC; ISSN: 0892-6638  
 PB Federation of American Societies for Experimental Biology  
 DT Journal; General Review  
 LA English

TI The nicotinamide dinucleotide **binding** motif: a comparison of nucleotide **binding** proteins

AB A review with 47 refs. Classical NAD (NAD+) **binding** proteins contain a .beta..alpha..beta..alpha..beta. unit. By comparing 14 such proteins, it is obsd. that an addnl. .beta. strand assoc. with this unit to form the core topol., the min. **structure** necessary to **bind** cofactor. Although the overall topologies of the cofactor **binding** domains of nicotinamide **binding** proteins vary, they all contain at least the core topol. The first 30-35 amino acids of the core topol., called the fingerprint region, are diagnostic for the presence of a dinucleotide **binding** fold. There are four characteristics of this fingerprint region: (1) a phosphate **binding** consensus sequence, GXGXXG, (2) six positions usually occupied by small hydrophobic amino acids, (3) a conserved, neg. charged residue (Glu or Asp) at the end of the second .beta. strand of the fingerprint region, and (4) a conserved pos. charged residue (Arg or Lys) at the beginning of the first .beta. strand of the fingerprint region. The core topologies of the classical nicotinamide **binding** proteins overlap well with root mean squared deviations of main chain atoms ranging from 0.7 to 4.7 .ANG.. A conserved interaction (found in 8 of the 12 classical nicotinamide **binding** proteins studied) between the cofactor and the protein is a hydrogen bond between the pyrophosphate oxygen of NAD(P)+ and the carboxy-terminal glycine of the phosphate **binding** helix, the first .alpha. helix of the .beta..alpha..beta..alpha..beta. unit. The classical nicotinamide **binding** proteins all **bind** their cofactor in the same location and orientation, with the cofactor itself adopting a similar extended conformation in every structure. Although obsd. less frequently than the classical fold, numerous nonclassical folding patterns are also used by proteins that **bind** NAD(P)+.

ST review nicotinamide dinucleotide **binding** motif protein

IT Phosphate group  
(**binding** site; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT **Conformation and Conformers**  
(nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT Molecular orientation  
(of cofactor; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT Proteins, specific or class  
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)  
(NAD-**binding**, nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT Enzymes  
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)  
(NAD-dependent, nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT Nucleotides, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)  
(~~di-~~, nicotinamide adenine-contg.; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT Protein sequences  
(homol., nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT 9001-48-3, Glutathione reductase 9001-60-9, Lactate dehydrogenase  
RL: BSU (Biological study, unclassified); MSC (Miscellaneous); PRP (Properties); BIOL (Biological study)  
(-like proteins; nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

IT 53-59-8, NADP 53-84-9, NAD  
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)  
(nicotinamide dinucleotide **binding** motif of nucleotide **binding** proteins)

L8 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1995:991855 CAPLUS

DN 124:78167

TI A tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)+-containing protein**

AU Lee, Bheong-Uk; Lee, Keesoo; Mendez, Jacqueline; Shimkets, Lawrence J.

CS Dep. Microbiol., Univ. Georgia, Athens, GA, 30602, USA

SO Genes & Development (1995), 9(23), 2964-73

CODEN: GEDEEP; ISSN: 0890-9369

PB Cold Spring Harbor Laboratory Press

DT Journal

LA English

TI A tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)+-containing protein**

AB CsgA is a cell surface protein that plays an essential role in tactile responses during Myxococcus xanthus fruiting body formation by producing the morphogenic C-signal. The primary amino acid sequence of CsgA exhibits homol. with members of the short-chain alc. dehydrogenase (SCAD) family and several lines of evidence suggest that NAD(P)+ **binding** is essential for biol. activity. First, the predicted CsgA secondary **structure** based on the 3.alpha./20.beta.-hydroxysteroid dehydrogenase crystal **structure** suggests that the amino-terminal portion of the **protein** contains an NAD(P)+ **binding** pocket. Second, strains with csgA alleles encoding amino acid substitutions T6A and R10A in the NAD(P)+ **binding** pocket failed to develop. Third, exogenous MalE-CsgA rescues csgA development,

whereas MalE-CsgA with the amino acid substitution CsgA T6A does not. Finally, csgA spore yield increased .apprx.20% when buffer contg. 100 nM of MalE-CsgA was supplemented with 10<sup>-</sup> .mu.M of NAD<sup>+</sup> or NADP<sup>+</sup>. Conversely, 10 .mu.M of NADH or NADPH delayed development for .apprx.24 h and depressed spore levels .apprx.10%. Together, these results argue that NAD(P)<sup>+</sup> **binding** is crit. for C-signaling. S135 and K155 are conserved amino acids in the catalytic domain of SCAD members. Strains with csgA alleles encoding the amino acid substitutions S135T or K155R failed to develop. Furthermore, a MalE-CsgA protein contg. CsgA S135T was not able to restore development to csgA cells. In conclusion, amino acids conserved in the coenzyme **binding** pocket and catalytic site are essential for C-signaling.

- IT Microorganism development  
Myxococcus xanthus  
Signal transduction, biological  
(a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)<sup>+</sup>**-contg. **protein**)
- IT Proteins, properties  
RL: PRP (Properties)  
(gene csaA; a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)<sup>+</sup>**-contg. **protein**)
- IT 142298-62-2, Short-chain alcohol dehydrogenase  
RL: BSU--(Biological study, unclassified); BIOL--(Biological study)  
(a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)<sup>+</sup>**-contg. **protein** homologous with short-chain alc. dehydrogenase)
- IT 172726-89-5, Protein (Myxococcus xanthus gene csgA)  
RL: PRP (Properties)  
(amino acid sequence; a tactile sensory system of Myxococcus xanthus involves an extracellular **NAD(P)<sup>+</sup>**-contg. **protein**)

L8 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2002 ACS  
AN 1995:567243 CAPLUS  
DN 123:193725

TI Ascorbate free radical reductase mRNA levels are induced by wounding  
AU Grantz, Alexander A.; Brummell, David A.; Bennett, Alan B.

CS Mann Laboratory, Univ. California, Davis, CA, 95616, USA

SO Plant Physiology (1995), 108(1), 411-18  
CODEN: PLPHAY; ISSN: 0032-0889

PB American Society of Plant Physiologists

DT Journal

LA English

AB A cDNA clone encoding ascorbate free radical (AFR) reductase (EC 1.6.5.4) was isolated from tomato (Lycopersicon esculentum Mill.) and its mRNA levels were analyzed. The cDNA encoded a deduced protein of 433 amino acids and possessed amino acid domains characteristic of FAD- and **NAD(P)H-binding proteins** but did not possess typical eukaryotic targeting sequences, suggesting that it encodes a cytosolic form of AFR reductase. Low-stringency genomic DNA gel blot anal. indicated that a single nuclear gene encoded this enzyme. Total ascorbate contents were greatest in leaves, with decreasing amts. in stems and roots and relatively const. levels in all stages of fruit. AFR reductase activity was inversely correlated with total ascorbate content, whereas the relative abundance of AFR reductase mRNA was directly correlated with enzyme activity in tissues examd. AFR reductase mRNA abundance increased dramatically in response to wounding, a treatment that is known to also induce ascorbate-dependent prolyl hydroxylation required for the accumulation of hydroxyproline-rich glycoproteins. In addn., AFR reductase may contribute to maintaining levels of ascorbic acid for protection against wound-induced free radical-mediated damage. Collectively, the results suggest that AFR reductase activity is regulated at the level of mRNA abundance by low ascorbate contents or by factors that promote ascorbate utilization.

L8 ANSWER 19 OF 30 CAPLUS COPYRIGHT 2002 ACS  
 AN 1995:430130 CAPLUS  
 DN 123:50672  
 TI The use of synthetic peptides for the investigation of components interaction in monooxygenase rabbit liver system  
 AU Kritsky, A. M.; Kanaeva, I. P.; Davydov, D. R.; Stepanova, N. V.; Bachmanova, G. I.  
 CS Institute Biomedical Chemistry, Russian Academy Medical Sciences, Moscow, 119832, Russia  
 SO Cytochrome P450 Int. Conf., 8th (1994), Meeting Date 1993, 477-80.  
 Editor(s): Lechner, Maria Celeste. Publisher: Libbey, Montrouge, Fr.  
 CODEN: 61COAX  
 DT Conference  
 LA English  
 AB Local homol. of NADPH-cytochrome P 450 reductase and cytochrome b5 amino acid sequences allowed the authors to presume structural similarity between the cytochrome c **binding** centers in cytochrome b5 and NADPH-cytochrome P 450 reductase (Davydov, D. R.; et al., 1992). On the basis of this presumption the peptide LEEHPGGEE was synthesized which simulates the part of the cytochrome b5 **binding** center with cytochrome c and cytochrome P 450. The peptide's influence on the NADPH-dependent benzphetamine-N-demethylation reaction in a monomeric sol. reconstituted system (MRS), contg. NADPH-cytochrome P 450 reductase, cytochrome P 450 2B4 (2B4) and cytochrome b5, was studied. The action of this **peptide** on NAD(P)H-cytochrome c reductase activities was studied in microsomes as well. It was shown that it inhibits these reactions, but the process is not highly specific.

L8 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2002 ACS  
 AN 1994:649166 CAPLUS  
 DN 121:249166  
 TI Flavodoxin and NADPH-flavodoxin reductase from Escherichia coli support bovine cytochrome P450c17 hydroxylase activities  
 AU Jenkins, Christopher M.; Waterman, Michael R.  
 CS Dep. Biochem., Vanderbilt Univ. Sch. Med., Nashville, TN, 37232-0146, USA  
 SO Journal of Biological Chemistry (1994), 269(44), 27401-8  
 CODEN: JBCHA3; ISSN: 0021-9258  
 DT Journal  
 LA English  
 AB Two sol. flavoproteins, purified from Escherichia coli cytosol and identified as flavodoxin and NADPH-flavodoxin (ferredoxin) reductase (flavodoxin reductase) have been found in combination to support the 17.alpha.-hydroxylase activities of heterologously expressed bovine 17.alpha.-hydroxylase cytochrome P 450 (P450c17). Phys. characteristics of the two flavoproteins including absorbance spectra, mol. wts., and amino-terminal sequences are identical with those reported previously for E. coli flavodoxin and flavodoxin reductase. Flavodoxin reductase, possessing FAD as a cofactor, is able to reconstitute P450c17 activities only in the presence of flavodoxin, an FMN-contg. **protein**, and NAD(P)H. Reducing equiv. are utilized more effectively from NADPH than NADH by flavodoxin reductase. E. coli flavodoxin **binds** P450c17 directly and with relatively high affinity (apparent  $K_s$  .apprx. 0.2 .mu.M) at low ionic strength, as evidenced by a change in spin state of the P450c17 heme iron upon titrn. with flavodoxin. This apparent spin shift is attenuated at moderate ionic strengths (100-200mM KCl). In addn., bovine P450c17 **binds** reversibly to flavodoxin Sepharose in an ionic strength-dependent manner. These data implicate charge pairing as being important for the interaction between flavodoxin and P450c17. The authors propose that the amino acid sequence similarity between E. coli flavodoxin-flavodoxin reductase and the putative FMN, FAD, and NAD(P)H **binding** regions of cytochrome P 450 reductase provides the basis for the reconstruction of P450c17 activities by this bacterial system.

L8 ANSWER 21 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1994:500887 CAPLUS

DN 121:100887

TI Human NAD(P)H:quinone oxidoreductase2. Gene **structure**, activity, and tissue-specific expression

AU Jaiswal, Anil K.

CS Dep. Pharmacol., Fox Chase Cancer Cent., Philadelphia, PA, 19111, USA

SO Journal of Biological Chemistry (1994), 269(20), 14502-8

CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

TI Human NAD(P)H:quinone oxidoreductase2. Gene **structure**, activity, and tissue-specific expression

AB Human NAD(P)H:quinone oxidoreductase2 (NQO2) gene, 1336 base pairs (bp) of the 5'-flanking region and 165 bp of the 3'-flanking region, have been sequenced. NQO2 gene is 20 kilobase pairs in length and has seven exons interrupted by six introns as compared to the previously cloned NQO1 gene which contains six exons. The 187 bp of the first exon in the NQO2 gene are noncoding and are absent in the NQO1 gene. The 92 bp of the second exon in the NQO2 gene corresponded to the first exon of the NQO1 gene and so on. The sizes and nucleotide sequences of exons 3-6 are highly conserved between NQO2 and NQO1 genes. The last exon in the NQO2 gene is 1603 bp shorter than the last exon of the NQO1 gene and encodes for 58 amino acids as compared to 101 amino acids encoded by the NQO1 gene. This makes NQO2 protein 43 amino acids shorter than the NQO1 protein. The high degree of conservation between NQO2 and NQO1 gene organization and sequence confirmed that NQO2 gene encodes for a second member of the NQO gene family in human. Nucleotide sequence anal. of the 5'-flanking region of the NQO2 gene revealed presence of four SP1 **binding** sites at positions -214, -170, -106, and -75, a single copy of the antioxidant response element (ARE) at nucleotide -936, and three copies of xenobiotic response element (XRE) at positions -708, -557, and -51. ARE and XRE elements have previously been found in the promoters of the NQO1 and glutathione S-transferase Ya subunit genes and mediate increases in their expression in response to polycyclic arom. compds., phenolic antioxidants, and 2,3,7,8-tetrachlorodibenzyo-p-dioxin (TCDD), resp. The NQO2 cDNA-derived protein in monkey kidney COS1 cells efficiently catalyzed nitroredn. of anti-tumor compd. CB10-200, an analog of nitrophenylaziridine. Northern blot anal. indicates that NQO2 gene is expressed in human heart, brain, lung, liver, and skeletal muscle but does not express in placenta. In contrast, the NQO1 gene was expressed in all human tissues. Large variations were noticed for expression of the NQO2 and NQO1 genes among various tissues. The 1336 bp of the 5'-flanking region of the NQO2 gene contg. ARE and XRE was found sufficient to increase expression of the CAT gene in response to .beta.-naphthoflavone and TCDD in transfected human hepatoblastoma (Hep-G2) cells.

IT **Protein sequences**

(of NAD(P)H:quinone oxidoreductase2, of human)

L8 ANSWER 22 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1993:468370 CAPLUS

DN 119:68370

TI Light activation and molecular-mass changes of NAD(P)-glyceraldehyde 3-phosphate dehydrogenase of spinach and maize leaves

AU Scagliarini, Sandra; Trost, Paolo; Pupillo, Paolo; Valenti, Vincenzo

CS Dip. Biol., Univ. Bologna, Bologna, I-40126, Italy

SO Planta (1993), 190(3), 313-19

CODEN: PLANAB; ISSN: 0032-0935

DT Journal

LA English

AB Light modulation of chloroplast glyceraldehyde 3-phosphate dehydrogenase (NAD(P)-GAPDH; Ec 1.2.1.13) has been investigated. Complete activation of NADPH-dependent activity was achieved at 25 W.m-2 photosynthetically



active radiation in spinach (*Spinacia oleracea*) and 100 W.m<sup>-2</sup> in maize (*Zea mays*) leaves. Light activation was stronger in spinach (5-fold on av.) than in maize (2-fold), which shows higher dark activity. The NADH dependent activity did not change appreciably. Several substrate activators can simulate in vitro the light effect with recovery of latent NADPH-dependent activity of spinach enzyme, but they are almost inactive with maize enzyme. A mixt. of activators has been devised to fully activate the spinach enzyme under most conditions. The NAD(P)-GAPDH protein can be resolved by rapid gel filtration (fast protein liq. chromatog.) into three conformers which have different mol. masses according to the light conditions. Enzyme from darkened leaves or chloroplasts, or DCMU-treated chloroplasts is mainly a 600-kDa regulatory form with low NADPH-dependent activity relative to NADH-activity. Enzyme from spinach leaves or chloroplasts during photosynthesis is mainly a 300-kDa oligomer, which along with the 600-kDa form also occurs in leaves of darkened maize. The conformer of illuminated maize leaves is mainly a 160-kDa species. Results are consistent with a model of NAD(P)-GAPDH freely interconvertible between protomers of the 160-kDa (or 300-kDa intermediate) form with high NADPH-activity, produced in the light by the action of thioredoxin and activating metabolites (spinach only), and a regulatory 600-kDa conformer with lower NADPH-activity produced in darkness or when photosynthesis is inhibited. This behavior is reminiscent of the in-vitro properties of purified enzyme; therefore it seems unlikely that NAD(P)-GAPDH in the chloroplast is part of a stable multienzyme complex or is bound to membranes.

L8 ANSWER 23 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1992:230592 CAPLUS

DN 116:230592

TI Characterization of an extremely thermostable glutamate dehydrogenase: a key enzyme in the primary metabolism of the hyperthermophilic archaeobacterium, *Pyrococcus furiosus*

AU Robb, Frank T.; Park, Jae Bum; Adams, Michael W. W.

CS Cent. Mar. Biotechnol., Univ. Maryland, Baltimore, MD, USA

SO Biochimica et Biophysica Acta (1992), 1120(3), 267-72

CODEN: BBACAQ; ISSN: 0006-3002

DT Journal

LA English

IT **Protein sequences**

(of NAD(P)-glutamate dehydrogenase N-terminus, of *Pyrococcus furiosus*)

IT **Conformation and Conformers**

(of NAD(P)-glutamate dehydrogenase, of *Pyrococcus furiosus*, extreme thermal stability of)

L8 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1992:122291 CAPLUS

DN 116:122291

TI Sequence of a cDNA encoding the bi-specific NAD(P)H-nitrate reductase from the tree *Betula pendula* and identification of conserved protein regions

AU Friemann, Andreas; Brinkmann, Klaus; Hachtel, Wolfgang

CS Bot. Inst., Univ. Bonn, Bonn, W-5300/1, Germany

SO Molecular and General Genetics (1991), 227(1), 97-105

CODEN: MGGEAE; ISSN: 0026-8925

DT Journal

LA English

AB Nitrate reductase (NR) assays revealed a bi-specific NAD(P)H-NR (EC 1.6.6.2.) to be the only nitrate-reducing enzyme in leaves of hydroponically grown birches. To obtain the primary structure of the NAD(P)H-NR, leaf poly (A)<sup>+</sup> mRNA was used to construct a cDNA library in the lambda gt11 phage. Recombinant clones were screened with heterologous gene probes encoding NADH-NR from tobacco and squash. A 3.0-kb cDNA was isolated which hybridized to a 3.2-kb mRNA whose level was

significantly higher in plants grown on nitrate than in those grown on ammonia. The nucleotide sequence of the cDNA comprises a reading frame encoding a protein of 898 amino acids which reveals 67%-77% identity with NADH-nitrate reductase sequences from higher plants. To identify conserved and variable regions of the multicenter electron-transfer protein a graphical evaluation of identities found in NR sequence alignments was carried out. Thirteen well-conserved sections exceeding a size of 10 amino acids were found in higher plant nitrate reductases. Sequence comparisons with related redox proteins indicate that about half of the conserved NR regions are involved in cofactor **binding**. The most striking difference in the birch NAD(P)H-NR sequence in comparison to NADH-NR sequences was found at the putative pyridine nucleotide **binding** site. Southern anal. indicates that the bi-specific NR is encoded by a single copy gene in birch.

IT **Protein sequences**

(of NAD(P)H nitrate reductase, of *Betula pendula*, complete)

L8 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1991:599825 CAPLUS

DN 115:199825

TI Cloning, nucleotide sequence, and transcriptional analysis of the NAD(P)-dependent cholesterol dehydrogenase gene from a *Nocardia* sp. and its hyperexpression in *Streptomyces* spp

AU Horinouchi, Sueharu; Ishizuka, Hiroshi; Beppu, Teruhiko

CS Fac. Agric., Univ. Tokyo, Tokyo, 113, Japan

SO Applied and Environmental Microbiology (1991), 57(5), 1386-93

CODEN: AEMIDF; ISSN: 0099-2240

DT Journal

LA English

AB NAD(P)-dependent cholesterol dehydrogenases [NAD(P)-CDH], which allow easier quantification of cholesterol by means of directly measuring the A340 of NAD(P), are useful for clin. purposes. The amino acid sequences of the NH2 terminus and the fragments obtained by CNBr decompn. of the NAD(P)-CDH from a *Nocardia* sp. were detd. for prepn. of synthetic oligonucleotides as hybridization probes. A 4.4-kbp BamHI fragment hybridizing to these probes was cloned on pUC19 in *Escherichia coli*. The nucleotide sequence together with the detd. amino acid sequences revealed that this enzyme consists of 364 amino acids (Mr, 39,792) and contains an NAD(P)-**binding** consensus sequence at its NH2-terminal portion. High-resoln. S1 nuclease mapping suggested that in NAD(P)-CDH of both *Nocardia* and *Streptomyces* spp. transcription initiates at the adenine residue, which is the first position of the translational initiation triplet (AUG) of this protein. The S1 mapping expts. also showed that cholesterol-dependent regulation in the *Nocardia* sp. occurred at the level of transcription. In *Streptomyces lividans* contg. the cloned fragment, however, this promoter was expressed constitutively. DNA manipulation of the cloned gene in *E. coli*, including the generation of a ribosome-**binding** sequence at an appropriate position by oligonucleotide-directed mutagenesis, led to prodn. of this protein in a very large amt. but in the enzymically inactive form of inclusion bodies. On the other hand, a *Streptomyces* host-vector system was successfully used for producing 40 times as much enzymically active NAD(P)-CDH as that produced by the original *Nocardia* sp.

IT **Protein sequences**

(of NAD(P)-dependent cholesterol dehydrogenase and precursor, of *Nocardia*, complete)

L8 ANSWER 26 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1990:92923 CAPLUS

DN 112:92923

TI Nucleotide and deduced amino acid sequence of a human cDNA (NQO2) corresponding to a second member of the NAD(P)H:quinone oxidoreductase gene family. Extensive polymorphism at the NQO2 gene locus on chromosome

- AU Jaiswal, Anil K.; Burnett, Paula; Adesnik, Milton; McBride, O. Wesley  
CS Med. Cent., New York Univ., New York, NY, 10016, USA  
SO Biochemistry (1990), 29(7), 1899-906  
CODEN: BICHAW; ISSN: 0006-2960  
DT Journal  
LA English  
IT **Protein sequences**  
(of **NAD(P)H** quinone dehydrogenase, of human,  
complete)  
IT 9032-20-6  
RL: PRP (Properties)  
(isoform to, human gene for, **structure** and mapping and  
polymorphism of)
- L8 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2002 ACS  
AN 1988:506976 CAPLUS  
DN 109:106976  
TI **Structure-function** relationship of **NAD(P)H**:quinone reductase:  
characterization of amino-terminal blocking group and essential tyrosine  
and lysine residues  
AU Haniu, Mitsuru; Yuan, Henry; Chen, Shiuan; Iyanagi, Takashi; Lee, Terry  
D.; Shively, John E.  
CS Div. Immunol., Beckman Res. Inst. City of Hope, Duarte, CA, 91010, USA  
SO Biochemistry (1988), 27(18), 6877-83  
CODEN: BICHAW; ISSN: 0006-2960  
DT Journal  
LA English  
TI **Structure-function** relationship of **NAD(P)H**:quinone reductase:  
characterization of amino-terminal blocking group and essential tyrosine  
and lysine residues  
AB The N-terminal-blocked **peptide** of rat liver **NAD(P)H**-quinone oxidoreductase [**NAD(P)H** dehydrogenase (quinone),  
DT-diaphorase] was detd. by amino acid sequence anal. and by mass  
spectrometry. The mature protein was composed of 273 amino acids and  
contained an acetylated N-terminus, which was not identified by previous  
cDNA anal. The enzyme was inactivated by p-nitrobenzenesulfonyl fluoride  
(NBSF) or 2,4,6-trinitrobenzenesulfonate (TNBS) with pseudo-1st-order  
kinetics. These studies suggest that essential tyrosine and lysine may be  
present in the active site of this enzyme. The NBSF inhibition was  
protected by 1-naphthol and 1-naphthylamine, but not by NAD. However,  
TNBS inhibition was not prevented by the naphthalene derivs. or NAD.  
Specific peptides labeled with NBSF or TNBS were isolated by HPLC and were  
sequenced. These analyses revealed that the NBSF-labeled tyrosine resides  
in a predominantly hydrophobic region and TNBS-labeled lysine in a  
predominantly hydrophilic region.  
IT **Protein sequences**  
(of **NAD(P)H** dehydrogenase (quinone), of rat liver,  
complete)
- L8 ANSWER 28 OF 30 CAPLUS COPYRIGHT 2002 ACS  
AN 1988:181215 CAPLUS  
DN 108:181215  
TI The primary **structure** of the mitochondrial energy-linked  
nicotinamide nucleotide transhydrogenase deduced from the sequence of cDNA  
clones  
AU Yamaguchi, Mutsuo; Hatefi, Youssef; Trach, Kathleen; Hoch, James A.  
CS Dep. Basic Clin. Res., Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA  
SO Journal of Biological Chemistry (1988), 263(6), 2761-7  
CODEN: JBCHA3; ISSN: 0021-9258  
DT Journal  
LA English  
TI The primary **structure** of the mitochondrial energy-linked  
nicotinamide nucleotide transhydrogenase deduced from the sequence of cDNA

clones

AB The amino acid sequence of the bovine mitochondrial nicotinamide nucleotide transhydrogenase, which catalyzes hydride ion transfer between NAD(H) and NADP(H) coupled to proton translocation across the mitochondrial inner membrane, was deduced from the corresponding cDNA. Two clones were isolated by screening a bovine phage  $\lambda$ gt10 cDNA library, using 2 synthetic oligonucleotides and a cDNA restriction fragment as probes. The inserts together covered 3105 base pairs of coding sequence, corresponding to 1035 amino acid residues. However, the reading frame at the 5' end was still open. N-terminal sequence anal. of the isolated enzyme indicated the presence of 8 addnl. residues. Thus, the mature transhydrogenase has 1043 amino acid residues and a calcd. mol. wt. of 109,212. The deduced amino acid sequence of the transhydrogenase contained the sequence of 4 tryptic peptides that had been isolated from the enzyme. Two of these were the peptides that had been used for construction of the oligonucleotide probes. The other two were tryptic peptides isolated after labeling the NAD-binding site of the transhydrogenase. The central region of the transhydrogenase (residues 420-850) is highly hydrophobic and contains  $\approx 14$  membrane-spanning segments. By comparison, the N- and the C-terminal regions of the enzyme, which contain the NAD- and the putative NADP-binding sites, resp., are relatively hydrophilic and are probably located outside the mitochondrial inner membrane on the matrix side. There is considerable homol. between the bovine enzyme and the Escherichia coli transhydrogenase (2 subunits,  $\alpha$  with Mr = 54,000 and  $\beta$  with Mr = 48,700), whose amino acid sequence has been detd. from the genes.

IT Gene and Genetic element, animal

RL: BIOL (Biological study)

(for nicotinamide nucleotide transhydrogenase, of cattle mitochondria, **structure** of)

IT Mitochondria

(nicotinamide and nucleotide transhydrogenase of, of cattle, **structure** of cDNA for)

IT Cattle

(nicotinamide nucleotide transhydrogenase of mitochondria of, **structure** of cDNA for)

IT **Protein sequences**

(of NAD(P) transhydrogenase, of cattle mitochondria, complete)

IT 9014-18-0, Nicotinamide nucleotide transhydrogenase

RL: PRP (Properties)

(of mitochondria of cattle, **structure** of cDNA for)

L8 ANSWER 29 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1987:454250 CAPLUS

DN 107:54250

TI Anion transport in rat brain mitochondria: fumarate uptake via the dicarboxylate carrier

AU Passarella, Salvatore; Atlante, Anna; Barile, Maria; Quagliariello, Ernesto

CS Cent. Stud. Mitochondri Metab., Univ. Bari, Bari, 70126, Italy

SO Neurochemical Research (1987), 12(3), 255-64

CODEN: NEREDZ; ISSN: 0364-3190

DT Journal

LA English

AB The penetration of fumarate into rat brain mitochondria was investigated, as required in brain ammoniogenesis. Mitochondria swelled in ammonium fumarate, and this swelling was increased by both phosphate (Pi) and malate. According to a carrier-mediated process, fumarate translocation, which occurs in exchange with intramitochondrial malate or Pi shows satn. characteristics. By photometrically investigating the kinetics of fumarate/malate, fumarate/Pi, and malate/Pi exchanges, different Km values were obtained (10, 22, and 250  $\mu$ M, resp.), whereas no significant difference was found for Vmax values (40 nmol NAD(P)

reduced/min/mg protein). This suggested that fumarate and malate share a single carrier to enter mitochondria, namely the dicarboxylate carrier. Both comparison made of the Vmax values and inhibition studies excluded a fumarate translocation via either the tricarboxylate carrier, whose occurrence in brain is here demonstrated, or oxodicarboxylate carrier. Kinetic investigation of the dicarboxylate translocator showed the existence of SH group(s) and metal ion(s) at or near the substrate-binding sites. The exptl. findings are discussed in the light of fumarate uptake in vivo in brain ammoniogenesis.

L8 ANSWER 30 OF 30 CAPLUS COPYRIGHT 2002 ACS

AN 1974:45176 CAPLUS

DN 80:45176

TI Glutamate dehydrogenase. Modification of the distribution of polyhexamers by coenzymes and specific effectors

AU Dessen, Philippe; Pantaloni, Dominique

CS Lab. Enzymol., CNRS, Gif-sur-Yvette, Fr.

SO European Journal of Biochemistry (1973), 39(1), 157-69

CODEN: EJBCAI; ISSN: 0014-2956

DT Journal

LA French

AB The effects of the coenzymes NAD(P) and NAD(P)H and the effectors ADP and GTP on the polyhexameric **structure** of pig liver glutamate dehydrogenase (EC 1.4.1.3) (I) was investigated. The increase in the dp of I with the **binding** of NAD(P)H was explained by a higher affinity of the coenzymes for the protomers which have an assocd. area compared to the protomers which have a free area. No variation was obsd. with NAD(P), ADP, or GTP alone. The formation of the **protein** .cntdot.GTP.cntdot.NAD(P)H ternary complex led to a complete depolymn. when the two ligands were in satg. concns. The systematic study of the variations of polymn. in terms of increasing concn. of NAD(P)H at const. concn. of GTP, or in terms of increasing concn. of GTP at const. concn. of NAD(P)H showed that the interaction between the two opposite protomers of two consecutive hexamers were responsible for the sigmoidal shape of the depolymn. curves. The reversibility of this effect by ADP was assigned to a competition between the **binding** of ADP and GTP.

IT 53-57-6 53-59-8 53-84-9 58-64-0, biological studies 58-68-4 86-01-1

RL: BIOL (Biological study)

(glutamate dehydrogenase polyhexameric **structure** in presence of)

IT 9029-12-3

RL: PRP (Properties)

(polyhexameric **structure** of, coenzymes and effectors in)

CAPLUS COPYRIGHT 2002 ACS

AN 1996:573121 CAPLUS

DN 125:240912

TI The nicotinamide dinucleotide binding motif: a comparison of nucleotide binding proteins

AU Bellamacina, Cornelia R.

CS Rosenstiel Basic Medical Sciences Research Center, Brandeis University, Waltham, MA, 02254-9110, USA

SO FASEB Journal (1996), 10(11), 1257-1269

CODEN: FAJOEC; ISSN: 0892-6638

PB Federation of American Societies for Experimental Biology

DT Journal; General Review

LA English

AB A review with 47 refs. Classical NAD (NAD<sup>+</sup>) binding proteins contain a .beta..alpha..beta..alpha..beta. unit. By comparing 14 such proteins, it is obsd. that an addnl. .beta. strand assoc. with this unit to form the core topol., the min. structure necessary to bind cofactor. Although the overall topologies of the cofactor binding domains of nicotinamide binding proteins vary, they all contain at least the core topol. The first 30-35 amino acids of the core topol., called the fingerprint region, are diagnostic for the presence of a dinucleotide binding fold. There are four characteristics of this fingerprint region: (1) a phosphate binding consensus sequence, GXGXXG, (2) six positions usually occupied by small hydrophobic amino acids, (3) a conserved, neg. charged residue (Glu or Asp) at the end of the second .beta. strand of the fingerprint region, and (4) a conserved pos. charged residue (Arg or Lys) at the beginning of the first .beta. strand of the fingerprint region. The core topologies of the classical nicotinamide binding proteins overlap well with root mean squared deviations of main chain atoms ranging from 0.7 to 4.7 .ANG.. A conserved interaction (found in 8 of the 12 classical nicotinamide binding proteins studied) between the cofactor and the protein is a hydrogen bond between the pyrophosphate oxygen of NAD(P)<sup>+</sup> and the carboxy-terminal glycine of the phosphate binding helix, the first .alpha. helix of the .beta..alpha..beta..alpha..beta. unit. The classical nicotinamide binding proteins all bind their cofactor in the same location and orientation, with the cofactor itself adopting a similar extended conformation in every structure. Although obsd. less frequently than the classical fold, numerous nonclassical folding patterns are also used by proteins that bind NAD(P)<sup>+</sup>.